```
=> d que
L1            38 SEA FILE=REGISTRY ABB=ON  PLU=ON  HKNQY/SQSP
L2            34 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1


=> d ibib abs hitrn 1-34

L2   ANSWER 1 OF 34  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2004:771063  HCAPLUS
DOCUMENT NUMBER:          141:255540
TITLE:                    Sorghum nucleic acids and encoded proteins and their
                          uses improvement of transgenic plants
INVENTOR(S):              Kovalic, David K.; Zhou, Yihua; Cao, Yongwei
PATENT ASSIGNEE(S):       USA
SOURCE:                   U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S.
                          Ser. No. 850,147, abandoned.
                          CODEN: USXXCO
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   13
PATENT INFORMATION:

     PATENT NO.           KIND   DATE         APPLICATION NO.          DATE
     ---------------      ----   --------     --------------------     --------
     US 2004172684         A1    20040902     US 2004-767701           20040129
     US 2004172684         A1    20040902     US 2004-767701           20040129
PRIORITY APPLN. INFO.:                        US 2000-684016       A2  20001010
                                              US 2001-850147       B2  20010508
                                              US 2004-767701       A   20040129
AB   Nucleotide sequences are provided for 31,563 nucleic acids in a cDNA
     library from sorghum tissue. The open reading frame in each recombinant
     polynucleotide sequence is identified by a combination of predictive and
     homol. based methods. Functions of polypeptides encoded by the
     polynucleotide sequences are determined using a hierarchical classification
     tool, termed FunCAT, for Functional Categories Annotation Tool.
     Functional assignments from five public classification schemes, GO_BP,
     GO_CC, GO_MF, KEGG, and EC, and one internal Monsanto classification
     scheme, POI, are also provided. The disclosed recombinant polynucleotides
     and recombinant polypeptides find use in production of transgenic plants to
     produce plants having improved properties. [This abstract record is one of
     13 records for this document necessitated by the large number of index
     entries required to fully index the document and publication system
     constraints.].
IT   753117-91-8
     RL: BSU (Biological study, unclassified); BUU (Biological use,
     unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
        (amino acid sequence; sorghum nucleic acids and encoded proteins and
        their uses improvement of transgenic plants)

L2   ANSWER 2 OF 34  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2004:663852  HCAPLUS
                            Correction of: 2004:546903
DOCUMENT NUMBER:          141:186007
                            Correction of: 141:83619
TITLE:                    Rice nucleic acid molecules and encoded proteins and
                          their uses for plant improvement
INVENTOR(S):              La Rosa, Thomas J.; Kovalic, David K.; Zhou, Yihua;
                          Cao, Yongwei; Wu, Wei; Boukharov, Andrey A.; Barbazuk,
```

Brad W.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S. Ser. No. 837,604.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 27
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004123343	A1	20040624	US 2003-437963		20030514
US 2004123343	A1	20040624	US 2003-437963		20030514
PRIORITY APPLN. INFO.:			US 2000-197872P	P	20000419
			US 2001-837604	A2	20010418
			US 2003-437963	A	20030514

AB The present invention provides 102,483 cDNA sequences and their encoded protein sequences from rice (Oryza sativa). Bioinformatic anal. identified putative functions and uses for the nucleic acids/polypeptides. The disclosed polynucleotides and polypeptides find use in production of transgenic plants to produce plants having improved properties. [This abstract record is one of forty-one records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **737288-08-3**, Protein (Oryza sativa clone x fragment)
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; rice nucleic acid mols. and encoded proteins and their uses for plant improvement)

L2 ANSWER 3 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:663841 HCAPLUS
Correction of: 2004:546893
DOCUMENT NUMBER: 141:185998
Correction of: 141:66308
TITLE: Rice nucleic acid molecules and encoded proteins and their uses for plant improvement
INVENTOR(S): La Rosa, Thomas J.; Kovalic, David K.; Zhou, Yihua; Cao, Yongwei; Wu, Wei; Boukharov, Andrey A.; Barbazuk, Brad W.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S. Ser. No. 837,604.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 27
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004123343	A1	20040624	US 2003-437963		20030514
US 2004123343	A1	20040624	US 2003-437963		20030514
PRIORITY APPLN. INFO.:			US 2000-197872P	P	20000419
			US 2001-837604	A2	20010418
			US 2003-437963	A	20030514

AB The present invention provides 102,483 cDNA sequences and their encoded protein sequences from rice (Oryza sativa). Bioinformatic anal.

identified putative functions and uses for the nucleic acids/polypeptides. The disclosed polynucleotides and polypeptides find use in production of transgenic plants to produce plants having improved properties. [This abstract record is one of forty-one records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **736257-67-3**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; rice nucleic acid mols. and encoded proteins and their uses for plant improvement)

L2 ANSWER 4 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:567036 HCAPLUS
DOCUMENT NUMBER: 141:66038
TITLE: Genome evolution in yeasts
AUTHOR(S): Dujon, Bernard; Sherman, David; Fischer, Gilles; Durrens, Pascal; Casaregola, Serge; Lafontaine, Ingrid; de Montigny, Jacky; Marck, Christian; Neuveglise, Cecile; Talla, Emmanuel; Goffard, Nicolas; Frangeul, Lionel; Aigle, Michel; Anthouard, Veronique; Babour, Anna; Barbe, Valerie; Barnay, Stephanie; Blanchin, Sylvie; Beckerich, Jean-Marie; Beyne, Emmanuelle; Bleykasten, Claudine; Boisrame, Anita; Boyer, Jeanne; Cattolico, Laurence; Confanioleri, Fabrice; de Daruvar, Antoine; Despons, Laurence; Fabre, Emmanuelle; Fairhead, Cecile; Ferry-Dumazet, Helene; Groppi, Alexis; Hantraye, Florence; Hennequin, Christophe; Jauniaux, Nicolas; Joyet, Philippe; Kachouri, Rym; Kerrest, Alix; Koszul, Romain; Lemaire, Marc; Lesur, Isabelle; Ma, Laurence; Muller, Heloise; Nicaud, Jean-Marc; Nikolski, Macha; Oztas, Sophie; Ozier-Kalogeropoulos, Odile; Pellenz, Stefan; Potier, Serge; Richard, Guy-Franck; Straub, Marie-Laure; Suleau, Audrey; Swennen, Dominique; Tekaia, Fredj; Wesolowski-Louvel, Micheline; Westhof, Eric; Wirth, Benedicte; Zeniou-Meyer, Maria; Zivanovic, Ivan; Bolotin-Fukuhara, Monique; Thierry, Agnes; Bouchier, Christiane; Caudron, Bernard; Scarpelli, Claude; Gaillardin, Claude; Weissenbach, Jean; Wincker, Patrick; Souciet, Jean-Luc
CORPORATE SOURCE: Unite de Genetique Moleculaire des Levures (URA and UFR 927 Universite Pierre et Marie Curie), Paris, 75724, Fr.
SOURCE: Nature (London, United Kingdom) (2004), 430(6995), 35-44
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Identifying the mechanisms of eukaryotic genome evolution by comparative genomics is often complicated by the multiplicity of events that have taken place throughout the history of individual lineages, leaving only distorted and superimposed traces in the genome of each living organism. The hemiascomycete yeasts, with their compact genomes, similar lifestyle and distinct sexual and physiol. properties, provide a unique opportunity to explore such mechanisms. The complete, assembled genome sequences of four yeast species are presented, selected to represent a broad evolutionary range within a single eukaryotic phylum, that after anal.

pr d to be molecularly as dive as the entire phylum of chordates. A
to of .apprx.24,200 novel gen were identified, the translation
pr cts of which were classifie together with Saccharomyces cerevisiae
pr ins into .apprx.4700 famili forming the basis for interspecific
co risons. Anal. of chromosom aps and genome redundancies reveal that
th ifferent yeast lineages hav volved through a marked interplay
be en several distinct mol. me anisms, including tandem gene repeat
fo tion, segmental duplication a massive genome duplication and
ex sive gene loss. The genome equence are deposited in
Ge nk/EMBL/DDBJ under accessio os. CR380947-CR380959 for C. glabrata,
CR 121-CR382126 for K. lactis, 382127-CR382132 for Y. lipolytica, and
CR 133-CR382139 for D. hanseni [This abstract record is one of four
re ds for this document necess ated by the large number of index entries
re red to fully index the docu nt and publication system constraints.].
IT **704826-27-7**
RL SU (Biological study, uncla fied); PRP (Properties); BIOL
(B gical study)
amino acid sequence; genome olution in yeasts based on complete
nome sequences from Candida labrata, Kluyveromyces lactis, Yarrowia
polytica, and Debaryomyces nsenii)

L2 AN R 5 OF 34 HCAPLUS COPYRIG 2004 ACS on STN
ACCESSI NUMBER: 2004:567023 CAPLUS
DOCUMEN UMBER: 141:66037
TITLE: Genome evolu n in yeasts
AUTHOR(S): Dujon, Berna Sherman, David; Fischer, Gilles;
Durrens, Pas ; Casaregola, Serge; Lafontaine,
Ingrid; de M igny, Jacky; Marck, Christian;
Neuveglise, ile; Talla, Emmanuel; Goffard, Nicolas;
Frangeul, Li el; Aigle, Michel; Anthouard, Veronique;
Babour, Anna Barbe, Valerie; Barnay, Stephanie;
Blanchin, Sy e; Beckerich, Jean-Marie; Beyne,
Emmanuelle; eykasten, Claudine; Boisrame, Anita;
Boyer, Jeanne Cattolico, Laurence; Confanioleri,
Fabrice; de uvar, Antoine; Despons, Laurence;
Fabre, Emman le; Fairhead, Cecile; Ferry-Dumazet,
Helene; Grop Alexis; Hantraye, Florence; Hennequin,
Christophe; niaux, Nicolas; Joyet, Philippe;
Kachouri, Ry Kerrest, Alix; Koszul, Romain; Lemaire,
Marc; Lesur, abelle; Ma, Laurence; Muller, Heloise;
Nicaud, Jean rc; Nikolski, Macha; Oztas, Sophie;
Ozier-Kaloge oulos, Odile; Pellenz, Stefan; Potier,
Serge; Richa Guy-Franck; Straub, Marie-Laure;
Suleau, Audr Swennen, Dominique; Tekaia, Fredj;
Wesolowski-L el, Micheline; Westhof, Eric; Wirth,
Benedicte; Z ou-Meyer, Maria; Zivanovic, Ivan;
Bolotin-Fuku a, Monique; Thierry, Agnes; Bouchier,
Christiane; dron, Bernard; Scarpelli, Claude;
Gaillardin, ude; Weissenbach, Jean; Wincker,
Patrick; Sou t, Jean-Luc
CORPORA SOURCE: Unite de Gen que Moleculaire des Levures (URA and
UFR 927 Univ site Pierre et Marie Curie), Paris,
75724, Fr.
SOURCE: Nature (Lond United Kingdom) (2004), 430(6995),
35-44
CODEN: NATUA ISSN: 0028-0836
PUBLISHE Nature Publi ng Group
DOCUMEN TYPE: Journal
LANGUAG English

AB Identifying the mechanisms of eukaryotic genome evolution by comparative genomics is often complicated by the multiplicity of events that have taken place throughout the history of individual lineages, leaving only distorted and superimposed traces in the genome of each living organism. The hemiascomycete yeasts, with their compact genomes, similar lifestyle and distinct sexual and physiol. properties, provide a unique opportunity to explore such mechanisms. The complete, assembled genome sequences of four yeast species are presented, selected to represent a broad evolutionary range within a single eukaryotic phylum, that after anal. proved to be molecularly as diverse as the entire phylum of chordates. A total of .apprx.24,200 novel genes were identified, the translation products of which were classified together with Saccharomyces cerevisiae proteins into .apprx.4700 families, forming the basis for interspecific comparisons. Anal. of chromosome maps and genome redundancies reveal that the different yeast lineages have evolved through a marked interplay between several distinct mol. mechanisms, including tandem gene repeat formation, segmental duplication, a massive genome duplication and extensive gene loss. The genome sequence are deposited in GenBank/EMBL/DDBJ under accession nos. CR380947-CR380959 for C. glabrata, CR382121-CR382126 for K. lactis, CR382127-CR382132 for Y. lipolytica, and CR382133-CR382139 for D. hansenii. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **704767-26-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome evolution in yeasts based on complete genome sequences from Candida glabrata, Kluyveromyces lactis, Yarrowia lipolytica, and Debaryomyces hansenii)

L2 ANSWER 6 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:489371 HCAPLUS
DOCUMENT NUMBER: 141:185815
TITLE: Genome compaction and stability in microsporidian intracellular parasites
AUTHOR(S): Slamovits, Claudio H.; Fast, Naomi M.; Law, Joyce S.; Keeling, Patrick J.
CORPORATE SOURCE: Canadian Institute for Advanced Research, Department of Botany, University of British Columbia, Vancouver, BC, V6T 1Z4, Can.
SOURCE: Current Biology (2004), 14(10), 891-896
CODEN: CUBLE2; ISSN: 0960-9822
PUBLISHER: Cell Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Microsporidian genomes are extraordinary among eukaryotes for their extreme reduction; although they are similar in form to other eukaryotic genomes, they are typically smaller than many prokaryotic genomes. At the same time, their rates of sequence evolution are among the highest for eukaryotic organisms. To explore the effects of compaction on nuclear genome evolution, we sequenced 685,000 bp of the Antonospora locustae genome (formerly Nosema locustae) and compared its organization with the recently completed genome of the human parasite Encephalitozoon cuniculi . Despite being very distantly related, the genomes of these two microsporidian species have retained an unexpected degree of synteny: 13% of genes are in the same context, and 30% of the genes were separated by a small number of short rearrangements. Microsporidian genomes are, therefore, paradoxically composed of rapidly evolving sequences harbored within a slowly evolving genome, although these two processes are sometimes

considered to be coupled . Microsporidian genomes show that eukaryotic genomes (like genes) do not evolve in a clock-like fashion, and genome stability may result from compaction in addition to a lack of recombination, as has been traditionally thought to occur in bacterial and organelle genomes .

IT **713041-08-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome compaction and stability in microsporidian intracellular parasites)

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:475863 HCAPLUS
DOCUMENT NUMBER: 141:2411
TITLE: Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics
INVENTOR(S): Weinstock, Keith G.; Bush, David
PATENT ASSIGNEE(S): Genome Therapeutics Corporation, USA
SOURCE: U.S., 872 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 6747137	B1	20040608	US 1999-248796		19990212
US 6747137	B1	20040608	US 1999-248796		19990212
PRIORITY APPLN. INFO.:			US 1998-74725P	P	19980213
			US 1998-96409P	P	19980813
			US 1999-248796	A	19990212

AB The invention provides isolated polypeptide and nucleic acid sequences derived from the genome of Candida albicans strain SC5314, which thus comprises a DNA sequence library of C. albicans genomic DNA and targets for therapeutic drugs. The 14,103 gene plus encoded protein sequences are useful in diagnosis and therapy of pathol. conditions, preparation of antibodies against the polypeptides, and in methods for the production of the polypeptides. The invention provides 8 preferred open reading frames: orf 970662_f3_3 (the homolog of Saccharomyces cerevisiae hypothetical 80.5-kDa protein in sin1-rad25 intergenic region); orf 480202_c3_10 (hypothetical 100.6 kDa protein in sin4-ure2 intergenic region); orf 24413557_f3_4 (probably membrane protein ylr001c); orf 4797561_c3_5 (agglutinin-like protein); orf 33595927_c3_19 (homolog of spac57a7.05 of Schizosaccharomyces pombe); orf 32116327_c2_18 (intracellular protein transport protein); orf 4720302_f1_1 (aluminum resistance protein); and orf 1173287_c3_18 (spa2 protein involved in cell polarity). The invention also provides methods for the detection, prevention, and treatment of pathol. conditions resulting from fungal infection. [This abstract record is one of seven records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **696986-77-3**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics)

L2 ANSWER 8 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:155818 HCAPLUS
DOCUMENT NUMBER: 140:194471
TITLE: Nucleic acids and encoded proteins associated with plants and their uses for plant improvement
INVENTOR(S): Liu, Jingdong; Zhou, Yihua; Kovalic, David K.; Screen, Steven E.; Tabaska, Jack E.; Cao, Yongwei
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 46
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004034888	A1	20040219	US 2003-425114	20030428
US 2004034888	A1	20040219	US 2003-425114	20030428
PRIORITY APPLN. INFO.:			US 1999-304517 B1	19990506
			US 2001-985678 B2	20011105
			US 2003-425114 A	20030428

AB This invention provides 36,564 polynucleotide sequences isolated from cDNA libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aesticum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum, Brassica napus, Gossypium hirsutum, Cucumis sativis, Lilium asiatic, Sorghum bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **662205-34-7**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and encoded proteins associated with plants and their uses for plant improvement)

L2 ANSWER 9 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:155817 HCAPLUS
DOCUMENT NUMBER: 140:194470
TITLE: Nucleic acids and encoded proteins associated with plants and their uses for plant improvement
INVENTOR(S): Liu, Jingdong; Zhou, Yihua; Kovalic, David K.; Screen, Steven E.; Tabaska, Jack E.; Cao, Yongwei
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 46

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004034888	A1	20040219	US 2003-425114	20030428
US 2004034888	A1	20040219	US 2003-425114	20030428
PRIORITY APPLN. INFO.:			US 1999-304517	B1 19990506
			US 2001-985678	B2 20011105
			US 2003-425114	A 20030428

AB This invention provides 36,564 polynucleotide sequences isolated from cDNA libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aesticum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum, Brassica napus, Gossypium hirsutum, Cucumis sativis, Lilium asiatic, Sorghum bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **661771-20-6**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and encoded proteins associated with plants and their uses for plant improvement)

L2 ANSWER 10 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:100903 HCAPLUS
DOCUMENT NUMBER: 140:140734
TITLE: Genes and markers associated with improved oil production in corn plants
INVENTOR(S): Laurie, Cathy C.; Ravanello, Monica; Savage, Thomas; Ledeaux, John R.; Rogers, James A.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 22 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004025202	A1	20040205	US 2003-389566	20030314
PRIORITY APPLN. INFO.:			US 2002-365301P	P 20020315
			US 2002-392018P	P 20020626

AB Polynucleotides that encode proteins associated with oil content in plants are useful in constructs to make transgenic plants, e.g., maize or soybean, with desirable oil content phenotype and progeny of any generation derived from the fertile transgenic plants. Markers associated with oil content QTL are useful in breeding for plants with desired oil content.

IT **649806-39-3**
RL: PRP (Properties)
(unclaimed protein sequence; genes and markers associated with improved

oil production in corn plants)

L2 ANSWER 11 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:857725 HCAPLUS
DOCUMENT NUMBER: 139:333862
TITLE: The genome sequence of the entomopathogenic bacterium Photorhabdus luminescens
AUTHOR(S): Duchaud, Eric; Rusniok, Christophe; Frangeul, Lionel; Buchrieser, Carmen; Givaudan, Alain; Taourit, Sead; Bocs, Stephanie; Boursaux-Eude, Caroline; Chandler, Michael; Charles, Jean-Francois; Dassa, Elie; Derose, Richard; Derzelle, Sylviane; Freyssinet, Georges; Gaudriault, Sophie; Medigue, Claudine; Lanois, Anne; Powell, Kerrie; Siguier, Patricia; Vincent, Rachel; Wingate, Vincent; Zouine, Mohamed; Glaser, Philippe; Boemare, Noel; Danchin, Antoine; Kunst, Frank
CORPORATE SOURCE: Laboratoire de Genomique des Microorganismes Pathogenes, Institut Pasteur, Paris, 75724, Fr.
SOURCE: Nature Biotechnology (2003), 21(11), 1307-1313
CODEN: NABIF9; ISSN: 1087-0156
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Photorhabdus luminescens is a symbiont of nematodes and a broad-spectrum insect pathogen. The complete genome sequence of strain TT01 is 5,688,987 base pairs (bp) long and contains 4839 predicted protein-coding genes. Strikingly, it encodes a large number of adhesins, toxins, hemolysins, proteases and lipases, and contains a wide array of antibiotic synthesizing genes. These proteins are likely to play a role in the elimination of competitors, host colonization, invasion and bioconversion of the insect cadaver, making P. luminescens a promising model for the study of symbiosis and host-pathogen interactions. Comparison with the genomes of related bacteria reveals the acquisition of virulence factors by extensive horizontal transfer and provides clues about the evolution of an insect pathogen. Moreover, newly identified insecticidal proteins may be effective alternatives for the control of insect pests. The genome sequence is deposited in GenBank/EMBL/DDBJ under accession number BX470251 and in the NCBI RefSeq database under accession number NC_005126.
IT **595510-66-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of the entomopathogenic bacterium Photorhabdus luminescens)
REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 12 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:417770 HCAPLUS
DOCUMENT NUMBER: 139:3260
TITLE: Peptides promoting cell adherence, growth and secretion
INVENTOR(S): Campbell, Robertl.; Heidaran, Mohammad; Spargo, Catherine A.; Wilkins, Jamie H.; Haaland, Perry D.
PATENT ASSIGNEE(S): Becton, Dickinson and Company, USA
SOURCE: PCT Int. Appl., 78 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003044045	A2	20030530	WO 2002-US37207	20021119
WO 2003044045	A3	20040805		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003162289	A1	20030828	US 2001-992124	20011119
EP 1465918	A2	20041013	EP 2002-803686	20021119
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
PRIORITY APPLN. INFO.:			US 2001-992124 A	20011119
			WO 2002-US37207 W	20021119

AB The present invention provides specific peptides identified as having cell adhesion, growth, expression or secretion-enhancing activities. Many of the peptides of the invention may be produced in large quantity by such means as chemical synthesis or recombinant DNA methodol. They may be non-specifically adsorbed, or chemical attached to a surface or, alternatively, formulated in a culture medium to produce the desired effect on cultured cells.

IT **532436-28-5P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(peptides promoting cell adherence, growth and secretion)

L2 ANSWER 13 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:334489 HCAPLUS
DOCUMENT NUMBER: 138:350272
TITLE: Human G protein-coupled receptor nGPCR-14, its protein and cDNA sequences, and their diagnostic and therapeutic uses for mental disorder
INVENTOR(S): Lind, Peter; Parodi, Luis A.; Vogeli, Gabriel; Wood, Linda S.
PATENT ASSIGNEE(S): Swed.
SOURCE: U.S. Pat. Appl. Publ., 153 pp., Cont.-in-part of U.S. Ser. No. 714,449.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003082534	A1	20030501	US 2001-782974	20010214
PRIORITY APPLN. INFO.:			US 1999-165838P P	19991116
			US 1999-166071P P	19991117
			US 1999-166678P P	19991119
			US 1999-173396P P	19991228
			US 2000-184129P P	20000222

US 2000-185421P	P	20000228
US 2000-185554P	P	20000228
US 2000-186530P	P	20000302
US 2000-186811P	P	20000303
US 2000-188114P	P	20000309
US 2000-190310P	P	20000317
US 2000-190800P	P	20000321
US 2000-198568P	P	20000420
US 2000-201190P	P	20000502
US 2000-203111P	P	20000508
US 2000-207094P	P	20000525
US 2000-714449	A2	20001116

AB The present application claims amino acid and cDNA sequences of human G protein-coupled receptor termed nGPCR-14. The invention provides constructs and recombinant host cells incorporating the genes, the nGPCR-x polypeptides encoded by the gene, antibodies to the nGPCR-x polypeptides, and methods of making and using all of the foregoing. The present invention provides a method of identifying a compound which modulates the activity of nGPCR-14. The present invention provides kit for screening a human subject to diagnose schizophrenia or a genetic predisposition therefor.

IT **518416-17-6**
RL: PRP (Properties)
(unclaimed protein sequence; human G protein-coupled receptor nGPCR-14, its protein and cDNA sequences, and their diagnostic and therapeutic uses for mental disorder)

L2 ANSWER 14 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:326608 HCAPLUS
DOCUMENT NUMBER: 138:298925
TITLE: Propionibacterium acnes genes and encoded protein sequences and their use in therapy and diagnosis of acne vulgaris
INVENTOR(S): Mitcham, Jennifer L.; Skeiky, Yasir A. W.; Persing, David H.; Bhatia, Ajay; Maisonneuve, Jean-Francois L.; Zhang, Yanni; Wang, Siqing; Jen, Shyian; Lodes, Michael J.; Benson, Darin R.; Jones, Robert; Carter, Darrick; Barth, Brenda; Vallieve-Douglass, John
PATENT ASSIGNEE(S): Corixa Corporation, USA
SOURCE: PCT Int. Appl., 1481 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 8
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003033515	A1	20030424	WO 2002-XD32727	20021011

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

WO 2003033515 A1 20030424 WO 2002-US32727 20021011
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2001-978825 A 20011015
WO 2002-US32727 A 20021011

AB Compns. and methods for the therapy and diagnosis of acne vulgaris and other related conditions are disclosed. The invention provides 299 contig sequences assembled from 56,716 fragments of the Propionibacterium acnes (strain ATCC 6919 or NCTC737) genome. Translation of all 299 contigs in all 6 possible reading frames identified 28,913 open reading frames at least 50 amino acids in length. BLAST and GenMark bioinformatic analyses were used to identify protein-coding regions from the DNA sequence. Re-anal. using Phrap reduced the number of contigs to 105, and identified 26,462 ORFs including an addnl. 1692 new putative ORFs. Several P. acnes antigens were identified by serol. expression cloning to be correlated with patients with histories of severe acnes. Given the importance of proteins as immunotherapeutic/vaccine targets, BLASTp and TBLASTN searches identified specific ORFs as members of the classes of transferase, enterotoxin, lipoprotein, membrane, permease, enterobactin, protease/proteinase, protein A, secreted, dismutase, adhesin, transporter, hemolysin, penicillin-binding protein, sialidase, siderophore, and lipase proteins. Therapeutic compns. may comprise one or more Propionibacterium acnes proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antibody that binds a Propionibacterium acnes protein, antigen-presenting cell that expresses a Propionibacterium acnes protein, or a T cell that is specific for cells expressing such a protein. Such compns. may be used, for example, for the prevention and/or treatment of acne. An animal model for P. acnes-induced inflammatory acne is also provided for identification of immunogenic proteins by serol. expression cloning and proteomic anal. [This abstract record is one of eight records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **510807-12-2**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; Propionibacterium acnes genes and encoded protein sequences and their use in therapy and diagnosis of acne vulgaris)

L2 ANSWER 15 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:315625 HCAPLUS
DOCUMENT NUMBER: 138:315855
TITLE: Identification and cloning of plant cinnamyl alcohol dehydrogenases
INVENTOR(S): Cahoon, Rebecca E.; Fader, Gary M.; Rafalski, J. Antoni
PATENT ASSIGNEE(S): E. I. Du Pont de Nemours & Co., USA
SOURCE: U.S., 47 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 6552249	B1	20030422	US 2000-501115		20000209
US 2003159170	A1	20030821	US 2003-357886		20030204
PRIORITY APPLN. INFO.:			US 1999-119585P	P	19990210
			US 2000-501115	A3	20000209

AB This invention relates to an isolated nucleic acid fragment encoding a lignin biosynthetic enzyme. The invention also relates to the construction of a chimeric gene encoding all or a portion of the lignin biosynthetic enzyme, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the lignin biosynthetic enzyme in a transformed host cell. Thus, cDNA fragments from rice, corn soybean, and wheat comprising cinnamyl alc. dehydrogenase genes cad1, cad2, cad3, cad4, and cad5, were identified and isolated from cDNA libraries of each plant.

IT **514229-58-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; identification and cloning of plant cinnamyl alc. dehydrogenases)

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:202782 HCAPLUS
DOCUMENT NUMBER: 138:233036
TITLE: Human lung-specific nucleic acids and proteins in normal and neoplastic tissues and their diagnostic and therapeutic uses
INVENTOR(S): Sun, Yongming; Liu, Chenghua; Chen, Sei-yu
PATENT ASSIGNEE(S): Diadexus, Inc., USA
SOURCE: PCT Int. Appl., 263 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003020899	A2	20030313	WO 2002-US27771	20020829
WO 2003020899	A3	20040226		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-316260P P 20010831

AB The present invention relates to 92 newly identified nucleic acid mols. and 86 polypeptides present in normal and neoplastic lung cells, including

fragments, variants and derivs. of the nucleic acids and polypeptides. Identification of the lung-specific genes was carried out by a systematic anal. of gene expression data in the LIFESEQ® Gold database available from Incyte Genomics Inc., using the data mining software package CLASP®. The CLASP target gene identification process is focused on, but no limited to, five CLASP profiles: tissue-specific expression, cancer-specific expression, differentially expressed in cancer, and maximum tissue differential expression. Gene expression in cancerous tissues was also analyzed using custom 60-mer oligonucleotide microarrays provided by Agilent Technologies, Inc. Chromosomal location assignments, and protein motifs/domains are also provided. The present invention also relates to antibodies to the polypeptides of the invention, as well as agonists and antagonists of the polypeptides of the invention. The invention, also relates to compns. containing the nucleic acid mols., polypeptides, antibodies, agonists and antagonists of the invention and methods for the use of these compns. These uses include identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous disease states in lung, identifying lung tissue, monitoring and identifying and/or designing agonists and antagonists of polypeptides of the invention. The uses also include gene therapy, production of transgenic animals and cells, and production of engineered lung tissue for treatment and research.

IT **501183-59-1P**
RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human lung-specific nucleic acids and proteins in normal and neoplastic tissues and their diagnostic and therapeutic uses)

L2 ANSWER 17 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:78650 HCAPLUS
DOCUMENT NUMBER: 138:249516
TITLE: Reductive genome evolution in Buchnera aphidicola
AUTHOR(S): Van Ham, Roeland C. H. J.; Kamerbeek, Judith; Palacios, Carmen; Rausell, Carolina; Abascal, Federico; Bastolla, Ugo; Fernandez, Jose M.; Jimenez, Luis; Postigo, Marina; Silva, Francisco J.; Tamames, Javier; Viguera, Enrique; Latorre, Amparo; Valencia, Alfonso; Moran, Federico; Moya, Andres
CORPORATE SOURCE: Centro de Astrobiologia, Instituto Nacional de Tecnica Aeroespacial-Consejo Superior de Investigaciones Cientificas, Madrid, 28850, Spain
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2003), 100(2), 581-586
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The genome of the intracellular symbiont Buchnera aphidicola from the aphid Baizongia pistacea was sequenced. This strain diverged 80-150 million years ago from the common ancestor of two previously sequenced Buchnera strains. Here, a field-collected, nonclonal sample of insects was used as source material for laboratory procedures. As a consequence, the genome assembly unveiled intrapopulational variation, consisting of .apprx.1200 polymorphic sites. Comparison of the 618-kb (kbp) genome with the two other Buchnera genomes revealed a nearly perfect gene-order conservation, indicating that the onset of genomic stasis coincided

closely with establishment of the symbiosis with aphids, .apprx.200 million years ago. Extensive genome reduction also predates the synchronous diversification of Buchnera and its host; but, at a slower rate, gene loss continues among the extant lineages. A computational study of protein folding predicts that proteins in Buchnera, as well as proteins of other intracellular bacteria, are generally characterized by smaller folding efficiency compared with proteins of free living bacteria. These and other degenerative genomic features are discussed in light of compensatory processes and theor. predictions on the long-term evolutionary fate of symbionts like Buchnera. The chromosome and plasmid sequences of Buchnera aphidicola are deposited in GenBank/EMBL/DDBJ under accession nos. AE016826 and AF492591, resp., and in the RefSeq database under accession number NC_004545.

IT **497909-37-2**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence and reductive genome evolution in Buchnera aphidicola)

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 18 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:906291 HCAPLUS
DOCUMENT NUMBER: 138:12036
TITLE: Sequence of the Photorhabdus luminescens strain TT01 genome and uses of its genes for biopesticide development
INVENTOR(S): Duchaud, Eric; Taorit, Sead; Glaser, Philippe; Frangeul, Lionel; Kunst, Frederik; Danchin, Antoine; Buchrieser, Carmen
PATENT ASSIGNEE(S): Institut Pasteur, Fr.; Centre National De La Recherche Scientifique
SOURCE: PCT Int. Appl., 1205 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002094867	A2	20021128	WO 2002-IB3040	20020207
WO 2002094867	C1	20030123		
WO 2002094867	A3	20031113		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2002094867	A2	20021128	WO 2002-XA3040	20020207
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,				

UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
WO 2002094867 A2 20021128 WO 2002-XB3040 20020207
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
EP 1379549 A2 20040114 EP 2002-751498 20020207
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.: FR 2001-1659 A 20010207
WO 2002-IB3040 A 20020207

AB The invention concerns the genomic sequence and nucleotide sequences coding for polypeptides of Photorhabdus luminescens. Of particular interest are polypeptides involved in operons of biosynthesis of antibiotics, or of toxins, or polypeptides exhibiting a toxin or antibiotic type activity capable of being used as pesticide, bactericide or fungicide. Genomic DNA libraries were constructed from P. luminescens TT01 in three vector systems: pcDNA2.1 (Invitrogen), pSYX34, and BAC vector pBeloBAC11. Shotgun sequencing allowed the assembly of 41 contigs, which could be reassembled into 9 contigs comprising the large majority of the P. luminescens genome. The invention also includes vectors comprising said sequences and cells or animals transformed by said vectors. [This abstract record is one of three records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **477373-11-8**
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; sequence of the Photorhabdus luminescens strain TT01 genome and uses of its genes for biopesticide development)

L2 ANSWER 19 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:752115 HCAPLUS
DOCUMENT NUMBER: 137:289734
TITLE: Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14
AUTHOR(S): Gardner, Malcolm J.; Shallom, Shamira J.; Carlton, Jane M.; Salzberg, Steven L.; Nene, Vishvanath; Shoaibi, Azadeh; Ciecko, Anne; Lynn, Jeffery; Rizzo, Michael; Weaver, Bruce; Jarrahi, Behnam; Brenner, Michael; Parvizi, Babak; Tallon, Luke; Moazzez, Azita; Granger, David; Fujii, Claire; Hansen, Cheryl; Pederson, James; Feldblyum, Tamara; Peterson, Jeremy; Suh, Bernard; Angiuoli, Sam; Pertea, Mihaela; Allen, Jonathan; Selengut, Jeremy; White, Owen; Cummings, Leda M.; Smith, Hamilton O.; Adams, Mark D.; Venter, J. Craig; Carucci, Daniel J.; Hoffman, Stephen L.; Fraser, Claire M.
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Nature (London, United Kingdom) (2002), 419(6906),

531-534
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The mosquito-borne malaria parasite Plasmodium falciparum kills an estimated 0.7-2.7 million people every year, primarily children in sub-Saharan Africa. Without effective interventions, a variety of factors-including the spread of parasites resistant to antimalarial drugs and the increasing insecticide resistance of mosquitoes-may cause the number of malaria cases to double over the next two decades. To stimulate basic research and facilitate the development of new drugs and vaccines, the genome of Plasmodium falciparum clone 3D7 has been sequenced using a chromosome-by-chromosome shotgun strategy. This report describes nucleotide sequences of chromosomes 10, 11 and 14, and a re-anal. of the chromosome 2 sequence. These chromosomes represent about 35% of the 23-megabase P. falciparum genome. The sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AE001362.2 (chromosome 2), AE014185 (chromosome 10), AE014186 (chromosome 11), and AE014187 (chromosome 14).
IT **465601-73-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14)
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 20 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:637835 HCAPLUS
DOCUMENT NUMBER: 137:181398
TITLE: Protein and cDNA sequences of human G protein-coupled receptor and its use in diagnosis of mental disorder
INVENTOR(S): Lind, Peter; Parodi, Luis A.; Vogeli, Gabriel; Wood, Linda S.
PATENT ASSIGNEE(S): Pharmacia & Upjohn Company, USA
SOURCE: PCT Int. Appl., 244 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002064789	A1	20020822	WO 2001-US4641	20010214
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1364013	A1	20031126	EP 2001-910628	20010214
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.: WO 2001-US4641 W 20010214
AB The present application provides a protein and cDNA sequences of human G

protein-coupled receptor termed nGPCR-14. The invention provides constructs and recombinant host cells incorporating the genes, the nGPCR-14 polypeptides encoded by the gene, antibodies to the nGPCR-x polypeptides, and methods of making and using all of the foregoing. The present invention provides a method of identifying a compound which modulates the activity of nGPCR-x. The present invention provides kit for screening a human subject to diagnose schizophrenia or a genetic predisposition therefor.

IT **451540-81-1**
RL: PRP (Properties)
(unclaimed protein sequence; protein and cDNA sequences of human G protein-coupled receptor and its use in diagnosis of mental disorder)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 21 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:511629 HCAPLUS
DOCUMENT NUMBER: 137:58382
TITLE: 50 Million years of genomic stasis in endosymbiotic bacteria
AUTHOR(S): Tamas, Ivica; Klasson, Lisa; Canbaeck, Bjoern; Naeslund, A. Kristina; Eriksson, Ann-Sofie; Wernegreen, Jennifer J.; Sandstroem, Jonas P.; Moran, Nancy A.; Andersson, Siv G. E.
CORPORATE SOURCE: Department of Molecular Evolution, Evolutionary Biology Center, University of Uppsala, Uppsala, Swed.
SOURCE: Science (Washington, DC, United States) (2002), 296(5577), 2376-2379
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Comparison of two fully sequenced genomes of Buchnera aphidicola, the obligate endosymbionts of aphids, reveals the most extreme genome stability to date: no chromosome rearrangements or gene acquisitions have occurred in the past 50-70 million years, despite substantial sequence evolution and the inactivation and loss of individual genes. In contrast, the genomes of their closest free-living relatives, Escherichia coli and Salmonella spp., are >2000-fold more labile in content and gene order. The genomic stasis of B. aphidicola, likely attributable to the loss of phages, repeated sequences, and recA, indicates that B. aphidicola is no longer a source of ecol. innovation for its hosts. The complete genome sequence of B. aphidicola strain isolated from Schizaphis graminum is available in GenBank under accession number AE013218.

IT **439062-62-1**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; comparison of genome of sequences from two strains of Buchnera aphidicola suggest genomic stasis in endosymbiotic bacteria)

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 22 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:173235 HCAPLUS
DOCUMENT NUMBER: 136:396929
TITLE: Reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes

INVENTOR(S): Venter, J. Craig; Ad[illegible]s, Mark; Li, Peter W. D.; Myers, Eugene W.
PATENT ASSIGNEE(S): PE Corporation (NY), [illegible]SA
SOURCE: PCT Int. Appl., 21 p[illegible]
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 10
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001071042	A2	20010927	WO 2001-XD9231	20010323
W: AE, AG, AL, AM, AT, AU, AZ, BA, [illegible], BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, [illegible], ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, [illegible], KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, [illegible], MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, [illegible], TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, [illegible], RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, [illegible], TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, [illegible], LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, [illegible], MR, NE, SN, TD, TG				
WO 2001071042	A2	20010927	WO 2001-US9231	20010323
WO 2001071042	A3	20030313		
W: AE, AG, AL, AM, AT, AU, AZ, BA, [illegible], BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, [illegible], ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, [illegible], KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, [illegible], MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, [illegible], TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, [illegible], RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, [illegible], TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, [illegible], LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, [illegible], MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: US 2000-191637P P 20000323
US 2000-614150 A 20000711
WO 2001-US9231 A 20010323

AB The present invention is based on the se[illegible]encing and assembly of the Drosophila melanogaster genome. The pre[illegible]nt invention provides the primary nucleotide sequence of a large p[illegible]tion of the Drosophila melanogaster genome in a series of genom[illegible] and predicted transcript sequences. This information is provided [illegible]n the form of genomic, transcript and protein sequence informat[illegible]n and can be used to generate nucleic acid detection reagents and kits [illegible]uch as nucleic acid arrays. Primary sequences are provided as contig[illegible]us strings in a computer-readable format and recorded on [illegible]edia such as floppy disks, hard disks, magnetic tape, CD-ROM, RAM, ROM a[illegible] hybrids of these categories. Genes/exons can be predicted, sequences [illegible]n be edited and homol. searches of target motifs can be conducted. [Thi[illegible] abstract record is one of ten records for this document necessitated b[illegible] the large number of index entries required to fully index the document and [illegible]ublication system constraints.].

IT **431529-36-1**
RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANS[illegible] (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; reagents and ki[illegible], such as nucleic acid arrays, for detecting the expression of over [illegible],000 Drosophila genes)

L2 ANSWER 23 OF 34 HCAPLUS COPYRIGHT 2004 [illegible]CS on STN
ACCESSION NUMBER: 2002:96393 HCAPLUS

DOCUMENT NUMBER: 137:1518
TITLE: Propionibacterium acnes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris
INVENTOR(S): Skeiky, Yasir A. W.; Persing, David H.; Mitcham, Jennifer L.; Wang, Siqing Steven; Bhatia, Ajay; L'Maisonneuve, Jean-Francois; Zhang, Yanni; Jen, Shyian; Carter, Darrick
PATENT ASSIGNEE(S): Corixa Corporation, USA
SOURCE: PCT Int. Appl., 1069 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001081581	A2	20011101	WO 2001-XC12865	20010420
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001081581	A2	20011101	WO 2001-US12865	20010420
WO 2001081581	A3	20020314		
WO 2001081581	C2	20030103		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:		
US 2000-199047P	P	20000421
US 2000-208841P	P	20000602
US 2000-216747P	P	20000707
WO 2001-US12865	W	20010420

AB Compns. and methods for the therapy and diagnosis of acne vulgaris and other related conditions are disclosed. Compns. may comprise one or more Propionibacterium acnes proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Thus, overlapping clones representing .apprx.8.6 full-length genome equivalent from a P. acnes genomic library were aligned to form 299 linear contigs. These 299 contigs represent a total assembled length of about 2,656,860 nucleotides covering >90% of the P. acnes genome. Six-frame translation is performed in order to predict 28,913 open reading frames encoding P. acnes polypeptide sequences ≥50 amino acids in length. A therapeutic composition may also comprise an antibody that binds a P. acnes protein, antigen-presenting cells that express a P. acnes protein, or a T cell that is specific for cells expressing such a protein. Such compns. may be used, for example, for the prevention and/or treatment of acne.

IT **432221-67-5**
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic

use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; Propionibacterium acnes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris)

L2 ANSWER 24 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:863067 HCAPLUS
DOCUMENT NUMBER: 136:335951
TITLE: Characterization of the Streptococcus gordonii chromosomal region immediately downstream of the glucosyltransferase gene
AUTHOR(S): Vickerman, M. M.; Minick, P. E.; Mather, N. M.
CORPORATE SOURCE: Department of Oral Surgery and Hospital Dentistry, School of Dentistry and Department of Microbiology and Immunology, School of Medicine, Indiana University, Indianapolis, IN, 46202, USA
SOURCE: Microbiology (Reading, United Kingdom) (2001), 147(11), 3061-3070
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The Streptococcus gordonii glucosyltransferase gene, gtfG, is pos. regulated by the upstream determinant rgg. In the present study, two ORFs, transcribed on the opposite DNA strand, were identified immediately downstream of gtfG. The first, designated dsg, shares a convergent putative transcriptional terminator with gtfG, and encodes a predicted 46 kDa transmembrane protein similar to the Yersinia enterocolitica TrsA involved in polysaccharide biosynthesis. Insertional inactivation of dsg resulted in only .apprx. 60% of the parental level of glucosyltransferase activity. The 870 bp gene 5' to dsg is similar to the gtfG regulatory determinant. Designated rggD, this rgg-like determinant downstream of gtfG encodes a putative 33.6 kDa cytoplasmic protein. Despite their sequence similarity, the functions of rgg and rggD appear specific. Strains in which rggD was insertionally inactivated and strains containing plasmid-borne rggD had parental levels of glucosyltransferase activity. Northern blot hybridization analyses showed .apprx. 1.3 kb dsg-specific and .apprx. 1.0 kb rggD-specific mRNA transcripts associated with this region; no polycistronic transcript was observed Although rgg-like gene products have been demonstrated to function as pos. transcriptional regulators of adjacent genes in several streptococcal species. Northern blot anal. suggested that rggD did not influence the transcription of dsg or the divergent downstream ylbN-like determinant under the conditions in the present study. Comparison of this S. gordonii chromosome region to other streptococcal genomes, which do not contain the rgg/rggD-flanked region involved in glucan synthesis, raised intriguing possibilities about the origins of this chromosomal region, and also suggested that rggD might regulate a distally located gene.
IT **190676-21-2**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; characterization of the Streptococcus gordonii chromosomal region immediately downstream of the glucosyltransferase gene)
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 25 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:804263 HCAPLUS

DOCUMENT NUMBER: 135:367541
TITLE: Comparative genomics of Listeria species
AUTHOR(S): Glaser, P.; Frangeul, L.; Buchrieser, C.; Rusniok, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, E.; de Duruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durant, L.; Dussurget, O.; Entian, K.-D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.; Jackson, D.; Jones, L.-M.; Kaerst, U.; Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nedjari, H.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.-C.; Purcell, R.; Remmel, B.; Rose, M.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.-A.; Voss, H.; Wehland, J.; Cossart, P.
CORPORATE SOURCE: Genomique des Microoganismes Pathogenes, Institut Pasteur, Paris, 75724, Fr.
SOURCE: Science (Washington, DC, United States) (2001), 294(5543), 849-852
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Listeria monocytogenes is a food-borne pathogen with a high mortality rate that has also emerged as a paradigm for intracellular parasitism. The genome sequences of L. monocytogenes (2,994,528 base pairs) and a nonpathogenic species, L. innocua (3,011,209 base pairs) are presented and compared. A large number of predicted genes encoding surface and secreted proteins, transporters, and transcriptional regulators were found, consistent with the ability of both species to adapt to diverse environments. The presence of 270 L. monocytogenes and 149 L. innocua strain-specific genes (clustered in 100 and 63 islets, resp.) suggests that virulence in Listeria results from multiple gene acquisition and deletion events.
IT **367996-64-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequences and comparative genomics of Listeria monocytogenes and Listeria innocua)
REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 26 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:704138 HCAPLUS
DOCUMENT NUMBER: 135:222172
TITLE: Mechanisms of evolution in Rickettsia conori and R. prowazeki
AUTHOR(S): Ogata, Hiroyuki; Audic, Stephanie; Renesto-Audiffren, Patricia; Fournier, Pierre-Edouard; Barbe, Valerie; Samson, Delphine; Roux, Veronique; Cossart, Pascale; Weissenbach, Jean; Claverie, Jean-Michel; Raoult, Didier
CORPORATE SOURCE: Information Genetique & Structurale, CNRS-AVENTIS UMR 1889, Marseille, 13402, Fr.
SOURCE: Science (Washington, DC, United States) (2001), 293(5537), 2093-2098
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Rickettsia conori is an obligate intracellular bacterium that causes Mediterranean spotted fever in humans. The 1,268,755-nucleotide complete genome sequence of R. conori, containing 1374 open reading frames, was determined
This genome exhibits 804 of the 834 genes of the previously determined R. prowazeki genome plus 552 supplementary open reading frames and a 10-fold increase in the number of repetitive elements. Despite these differences, the two genomes exhibit a nearly perfect colinearity that allowed the clear identification of different stages of gene alterations with gene remnants and 37 genes split in 105 fragments, of which 59 are transcribed. A 38-kb sequence inversion was dated shortly after the divergence of the genus. The genome sequence of R. conori is deposited in GenBank under accession AE006914.
IT **359482-60-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Rickettsia conori and mechanisms of evolution in R. conori and R. prowazeki)
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 27 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:380635 HCAPLUS
DOCUMENT NUMBER: 134:362237
TITLE: Novel G protein-coupled receptors identified by sequence homology
INVENTOR(S): Vogeli, Gabriel; Wood, Linda S.; Parodi, Luis A.; Hiebsch, Ronald R.; Lind, Peter; Slightom, Jerry; Schellin, Kathleen A.; Kaytes, Paul S.; Bannigan, Christopher M.; Ruff, Valerie; Sejlitz, Torsten; Huff, Rita M.
PATENT ASSIGNEE(S): Pharmacia & Upjohn Co., USA
SOURCE: PCT Int. Appl., 261 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001036473	A2	20010525	WO 2000-US31581	20001116
WO 2001036473	A3	20020711		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1237909	A2	20020911	EP 2000-978750	20001116
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
AU 2001016178	A5	20010530	AU 2001-16178	20001117

PRIORITY APPLN. INFO.:

US 1999-165838P	P	19991116
US 1999-166071P	P	19991117
US 1999-166678P	P	19991119
US 1999-173396P	P	19991228
US 2000-184129P	P	20000222
US 2000-185421P	P	20000228
US 2000-185554P	P	20000228
US 2000-186530P	P	20000302
US 2000-186811P	P	20000303
US 2000-188114P	P	20000309
US 2000-190310P	P	20000317
US 2000-190800P	P	20000321
US 2000-198568P	P	20000420
US 2000-201190P	P	20000502
US 2000-203111P	P	20000508
US 2000-207094P	P	20000525
WO 2000-US31581	W	20001116

AB The present invention provides a gene encoding a G protein-coupled receptor termed nGPCR-x; constructs and recombinant host cells incorporating the genes; the beGPCR-x polypeptides encoded by the gene; antibodies to the beGPCR-x polypeptides; and methods of making and using all of the foregoing. Novel G protein-coupled receptors (GPCRs) that may be of use in the diagnosis or treatment of disease are identified by sequence homol. Candidate sequences were identified by BLAST querying a proprietary DNA sequence database for GPCR-like sequences. Candidate sequences were cloned and sequenced.

IT **340200-07-9**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; novel G protein-coupled receptors identified by sequence homol.)

L2 ANSWER 28 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:673694 HCAPLUS
DOCUMENT NUMBER: 133:218312
TITLE: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS
AUTHOR(S): Shigenobu, Shuji; Watanabe, Hidemi; Hattori, Masahira; Sakaki, Yoshlyukl; Ishikawa, Hajime
CORPORATE SOURCE: Department of Biological Sciences, Graduate School of Science, University of Tokyo, Tokyo, 113-0033, Japan
SOURCE: Nature (London) (2000), 407(6800), 81-86
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Almost all aphid species (Homoptera, Insecta) have 60-80 huge cells called bacteriocytes, within which are round-shaped bacteria that are designated Buchnera. These bacteria are maternally transmitted to eggs and embryos through host generations, and the mutualism between the host and the bacteria is so obligate that neither can reproduce independently. Buchnera is a close relative of Escherichia coli, but it contains more than 100 genomic copies per cell, and its genome size is only a seventh of that of Escherichia coli. The complete genome sequence of Buchnera sp. strain APS is now reported, which is composed of one 640,681-bp chromosome and two small plasmids. There are genes for the biosyntheses of amino acids essential for the hosts in the genome, but those for non-essential amino acids are missing, indicating complementarity and syntrophy between the host and the symbiont. In addition, Buchnera lacks genes for the

biosynthesis of cell-surface components, including lipopolysaccharides and phospholipids, regulator genes and genes involved in defense of the cell. These results indicate that Buchnera is completely symbiotic and viable only in its limited niche, the bacteriocyte.

IT **291590-51-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS)

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 29 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:630783 HCAPLUS
DOCUMENT NUMBER: 133:293271
TITLE: A homologue of the cell cycle check point TOR2 from Saccharomyces cerevisiae exists in the arbuscular mycorrhizal fungus Glomus mosseae
AUTHOR(S): Requena, Natalia; Mann, Petra; Franken, Philipp
CORPORATE SOURCE: Max-Planck-Institut fur terrestrische Mikrobiologie, Marburg, D-35043, Germany
SOURCE: Protoplasma (2000), 212(1-2), 89-98
CODEN: PROTA5; ISSN: 0033-183X
PUBLISHER: Springer-Verlag Wien
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A homolog of the gene TOR2 from Saccharomyces cerevisiae has been found in the arbuscular mycorrhizal (AM) fungus Glomus mosseae (BEG 12) during a differential RNA display experiment Further downstream sequence was obtained by a nested-PCR approach. Eight introns were found in 2.6 kb sequence. The fragment encodes a putative protein with high homol. (53% identity) to the C terminus of S. cerevisiae TOR2 and its homologues in Schizosaccharomyces pombe and humans. The gene was named GmTOR2. The expression of the gene was studied by reverse transcriptase-polymerase chain reaction and it was found to be expressed at a relatively high level during all the different life cycle stages of the AM fungus. TOR2 is known to be involved in the control of the cell cycle in S. cere isiae and the organization of the actin cytoskeleton in response to nutrients. The anti-inflammatory drug rapamycin, known to interfere with the role of TOR2 controlling the arrest of the cell cycle in G1 but not with its signalling to the actin cytoskeleton, was found to decrease hyphal growth of G. mosseae sporocarps but not to affect spore germination. This result confirms that DNA replication is not needed for germination but during the presymbiotic growth. The immunostaining of germinated sporocarps of G. mosseae with antibodies against tubulin showed the presence of mitotic spindles in some secondary spores, confirming previous findings of DNA replication during presymbiosis. The possibility that GmTOR2 controls the cell cycle arrest in AM fungi in the absence of the plant as a response to nutrient starvation is discussed.

IT **300624-99-1**
RL: PRP (Properties)
(amino acid sequence; homolog of cell cycle check point TOR2 from Saccharomyces cerevisiae exists in arbuscular mycorrhizal fungus Glomus mosseae)

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 30 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:282531 HCAPLUS

DOCUMENT NUMBER: 133:188719
TITLE: Purification, characterization, and molecular analysis of the gene encoding glucosyltransferase from Streptococcus oralis
AUTHOR(S): Fujiwara, Taku; Hoshino, Tomonori; Ooshima, Takashi; Sobue, Shizuo; Hamada, Shigeyuki
CORPORATE SOURCE: Departments of Pedodontics, Osaka University Faculty of Dentistry, Suita, 565-0871, Japan
SOURCE: Infection and Immunity (2000), 68(5), 2475-2483
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Streptococcus oralis is a member of the oral streptococcal family and an early-colonizing microorganism in the oral cavity of humans. S. oralis is known to produce glucosyltransferase (GTase), which synthesizes glucans from sucrose. The enzyme was purified chromatog. from a culture supernatant of S. oralis ATCC 10557. The purified enzyme, GTase-R, had a mol. mass of 173 kDa and a pI of 6.3. This enzyme mainly synthesized water-soluble glucans with no primer dependency. The addition of GTase markedly enhanced the sucrose-dependent resting cell adhesion of Streptococcus mutans at a level similar to that found in growing cells of S. mutans. The antibody against GTase-R inhibited the glucan-synthesizing activities of Streptococcus gordonii and Streptococcus sanguis, as well as S. oralis. The N-terminal amino acid sequence of GTase-R exhibited no similarities to known GTase sequences of oral streptococci. Using degenerate PCR primers, an 8.1-kb DNA fragment, carrying the gene (gtfR) coding for GTase-R and its regulator gene (rgg), was cloned and sequenced. Comparison of the deduced amino acid sequence revealed that the rgg genes of S. oralis and S. gordonii exhibited a close similarity. The gtfR gene was found to possess a species-specific nucleotide sequence corresponding to the N-terminal 130 amino acid residues. Insertion of erm or aphA into the rgg or gtfR gene resulted in decreased GTase activity by the organism and changed the colony morphol. of these transformants. These results indicate that S. oralis GTase may play an important role in the subsequent colonizing of mutans streptoccoci.

IT **288882-04-2**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; characterization, and mol. anal. of gene encoding glucosyltransferase from S. oralis)

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 31 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:270891 HCAPLUS
DOCUMENT NUMBER: 133:172863
TITLE: The division and cell wall gene cluster of Enterococcus hirae S185
AUTHOR(S): Duez, C.; Thamm, I.; Sapunaric, F.; Coyette, J.; Ghuysen, J. M.
CORPORATE SOURCE: Centre d'Ingenierie des Proteines, Universite de Liege, Institut de Chimie, Liege, B-4000, Belg.
SOURCE: DNA Sequence (1998), 9(3), 149-161
CODEN: DNSEES; ISSN: 1042-5179
PUBLISHER: Harwood Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A chromosomal 10355-bp segment of Enterococcus hirae S185 contains nine orfs which occur in the same order as the MraW-, FtsL-, PBP3-, MraY-, MurD-, MurG-, FtsQ-, FtsA- and FtsZ-encoding genes of the division and cell wall clusters of Escherichia coli and Bacillus subtilis. The E. hirae DNA segment lacks the genes which in E. coli encode the ligases Ddl, MurC, MurE and MurF and the integral membrane protein FtsW. The encoded E. hirae and E. coli proteins share 25% to 50% identity except FtsL and FtsQ (.simeq. 14% identity).

IT **288411-67-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; division and cell wall gene cluster of Enterococcus hirae S185)

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 32 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:246848 HCAPLUS
DOCUMENT NUMBER: 132:289494
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei,

Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBast at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **263489-54-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

L2 ANSWER 33 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:315983 HCAPLUS
DOCUMENT NUMBER: 127:29844
TITLE: Nucleotide sequence analysis of the Streptococcus gordonii glucosyltransferase gene, gtfG
AUTHOR(S): Vickerman, M. M.; Sulavik, M. C.; Nowak, J. D.; Gardner, N. M.; Jones, G. W.; Clewell, D. B.
CORPORATE SOURCE: Dep. Microbiol. Immunol., Sch. Med., Univ. Michigan, Ann Arbor, MI, 48109-0620, USA
SOURCE: DNA Sequence (1997), 7(2), 83-95
CODEN: DNSEES; ISSN: 1042-5179
PUBLISHER: Harwood
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Streptococcus gordonii has an extracellular glucosyltransferase (GTF) that polymerizes the glucose moiety of sucrose to form both water-soluble and water-insol. glucans. Whereas multiple gtf genes have been identified in strains of mutans streptococci and Streptococcus salivarius, a single gene, designated gtfG, encodes the GTF of S. gordonii Challis. GtfG is also unique among the characterized gtfs in that it has a described regulatory determinant, rgg. Furthermore, the GTF activity in S. gordonii undergoes reversible phase variation between high and low levels. To gain insight into this novel GTF system, the nucleotide sequence of gtfG was determined and found to consist of a 4,734 base pair open reading frame encoding a protein with a deduced mol. weight of .apprx.174,000. GtfG was similar to other sequenced gtfs with a conserved signal sequence followed by a .apprx.600-bp region distinctive for gtfG, a conserved region encoding a putative catalytic active site and a series of six direct repeats in the carboxyl terminal region implicated in glucan binding. Although comparison of gtfG to other gtfs did not show a basis for the primer-independence of the encoded enzyme or the nature of the glucan products, the gtfG sequence data provide as important basis for further studies of these enzymes.

IT **190676-21-2**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; nucleotide sequence anal. of the Streptococcus gordonii glucosyltransferase gene gtfG)

REFERENCE COUNT: 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 34 OF 34 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1995:715587 HCAPLUS
DOCUMENT NUMBER: 123:331364
TITLE: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
AUTHOR(S): Bork, Peer; Quzounis, Christos; Casari, Georg; Schneider, Reinhard; Sander, Chris; Dolan, Maureen; Gilbert, Walter; Gillevet, Pat M.
CORPORATE SOURCE: EMBL, Heidelberg, D-69012, Germany
SOURCE: Molecular Microbiology (1995), 16(5), 955-67
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We report on the anal. of 214kb of the parasitic eubacterium Mycoplasma capricolum sequenced by genomic walking techniques. The 287 putative proteins detected to date represent about half of the estimated total number of 500 predicted for this organism. A large fraction of these (75%) can be assigned a likely function as a result of similarity searches. Several

important features of the functional organization of this small genome are already apparent. Among these are (i) the expected relatively large number of enzymes involved in metabolic transport and activation, for efficient use of host cell nutrients; (ii) the presence of anabolic enzymes; (iii) the unexpected diversity of enzymes involved in DNA replication and repair; and (i.v.) a sizeable number of orthologs (82 so far) in Escherichia coli. This survey is beginning to provide a detailed view of how M. capricolum manages to maintain essential cellular processes with a genome much smaller than that of its bacterial relatives.

IT **170619-82-6**

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)

(amino acid sequence; DNA sequence of Mycoplasma capricolum genome in relation to cell physiol.)